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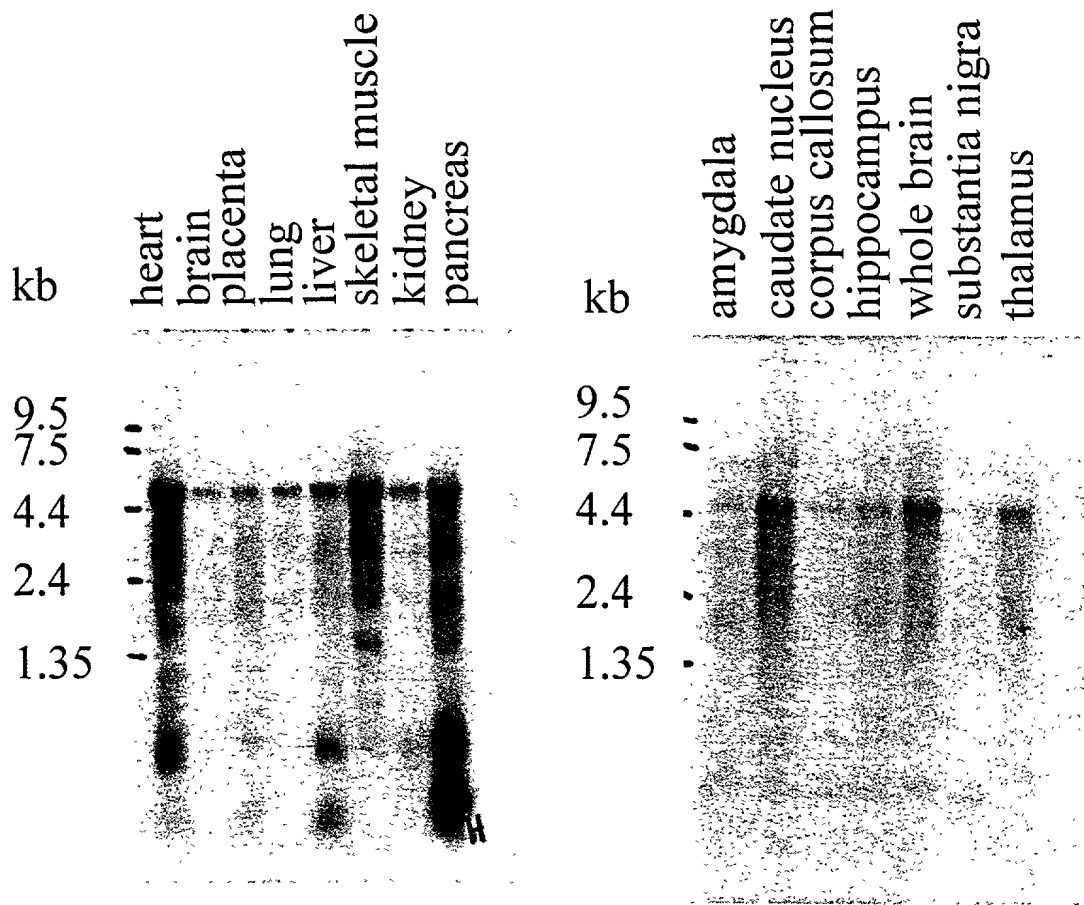


Fig. 1

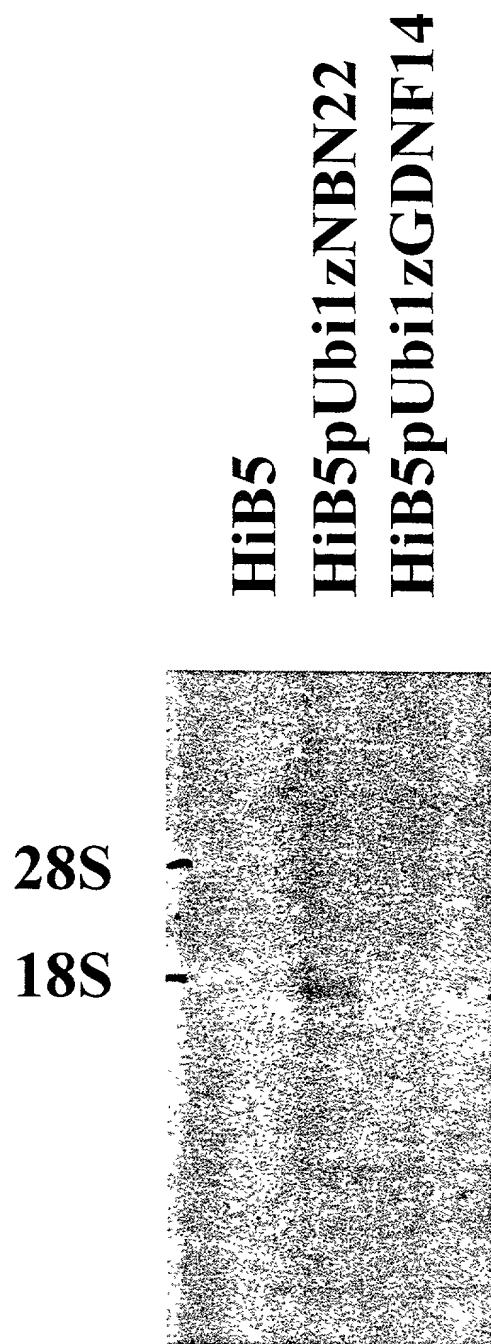


Fig. 2

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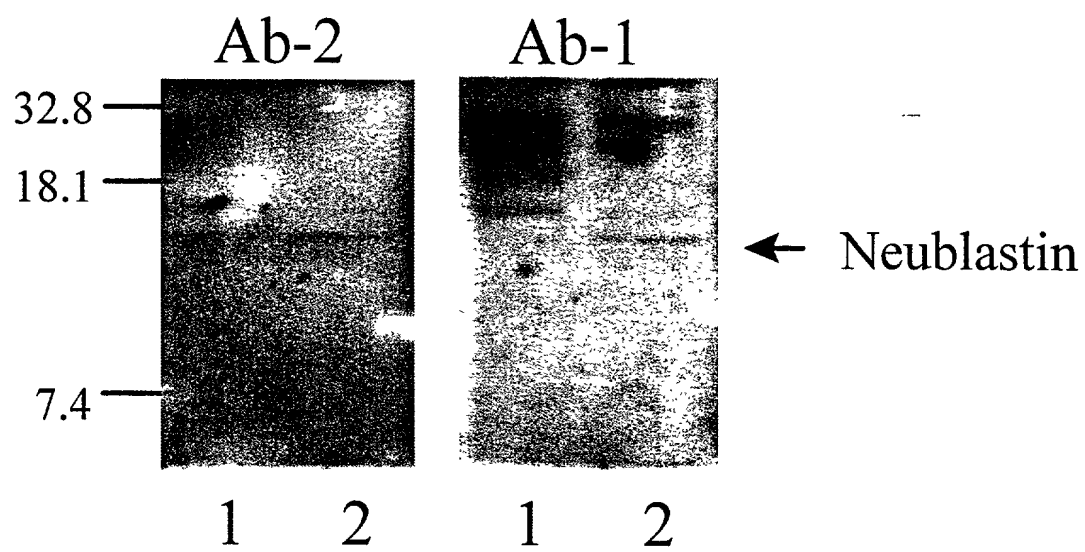
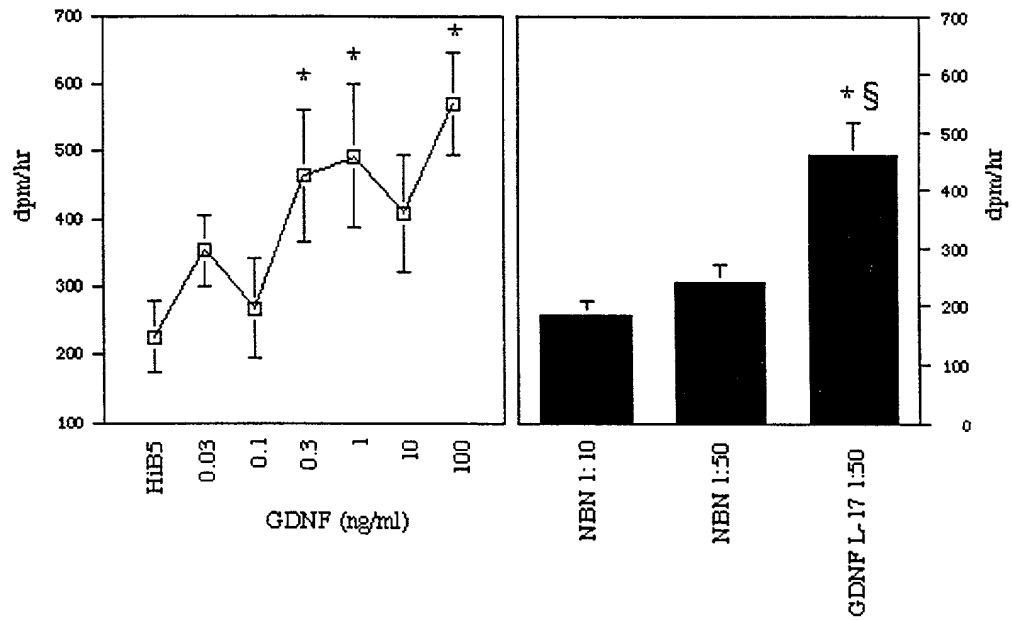
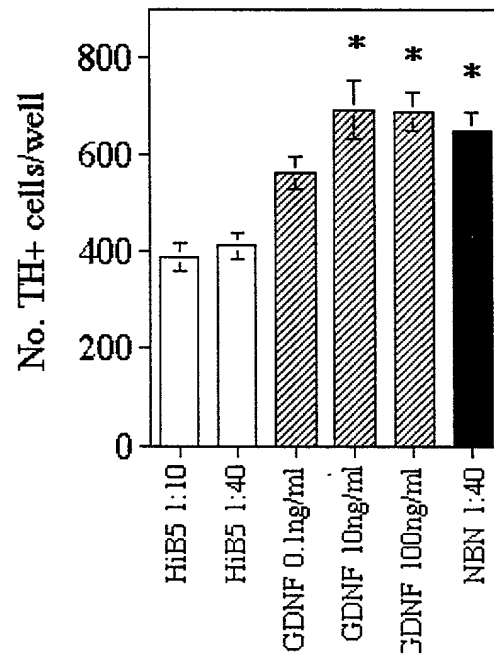


Fig. 3

NBN1 ChAT bioassay



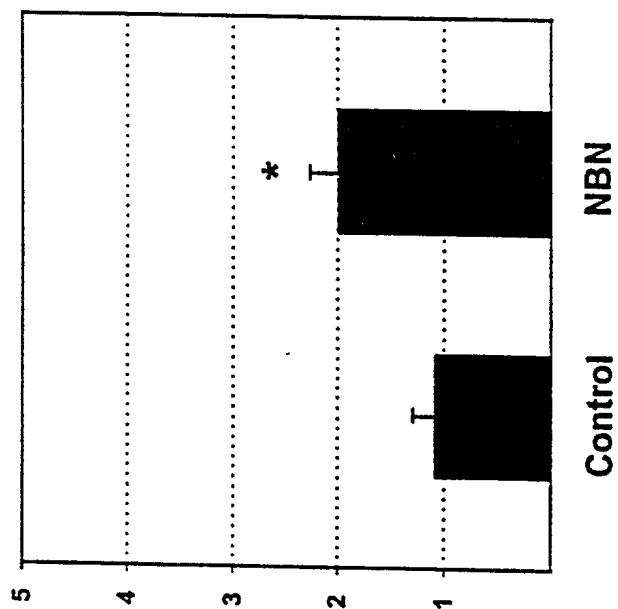
TH+ cell number at DIV 7



Figs. 4A, 4B and 4C

57118

Dopamine (pmol/ml) - day 12



Dopamine (pmol/ml) - day 21

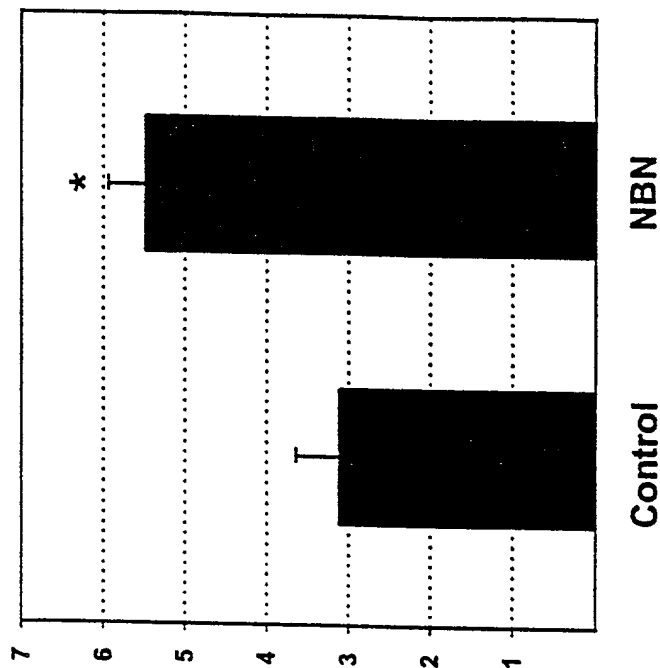


Fig. 5A and 5B

6118

TH-ir cells per culture

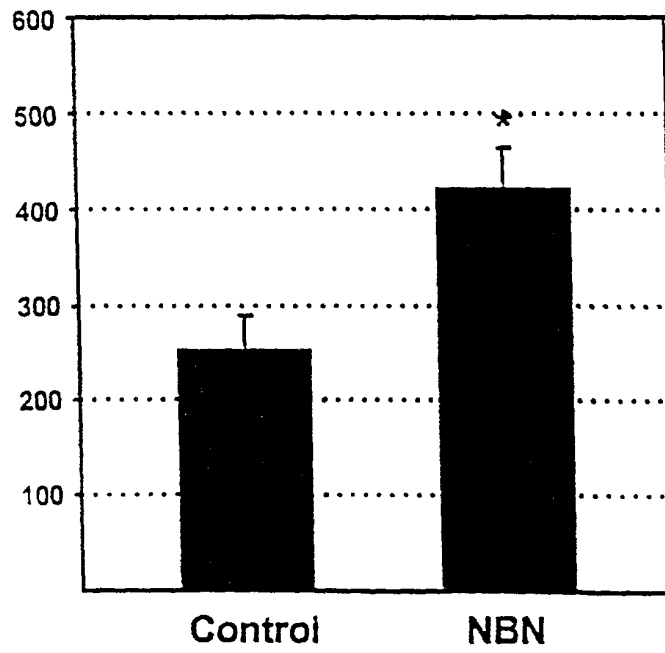


Fig. 5C

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%FG lesion/intact

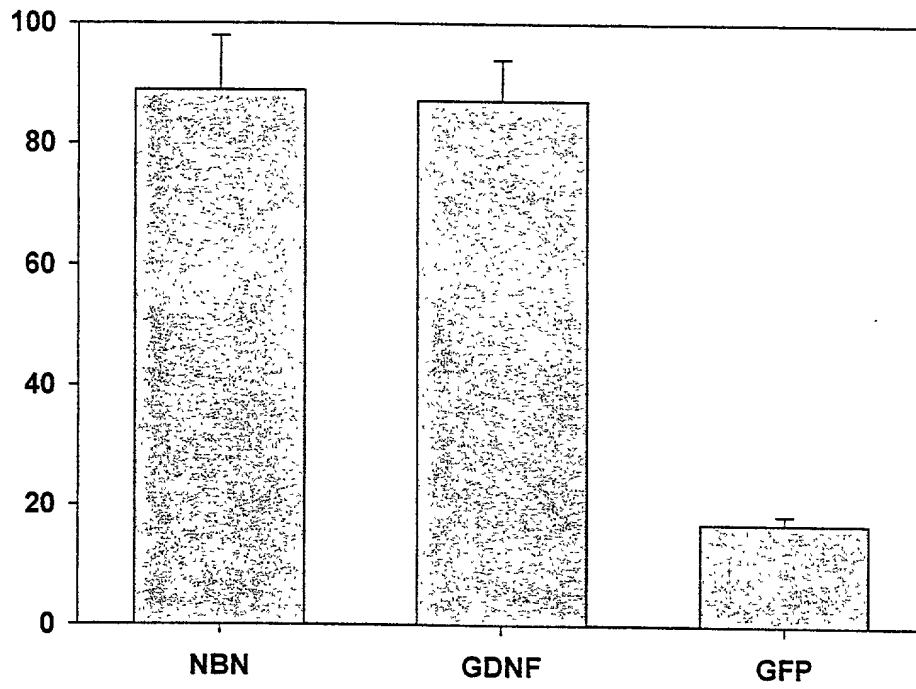


Fig. 6

8118
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

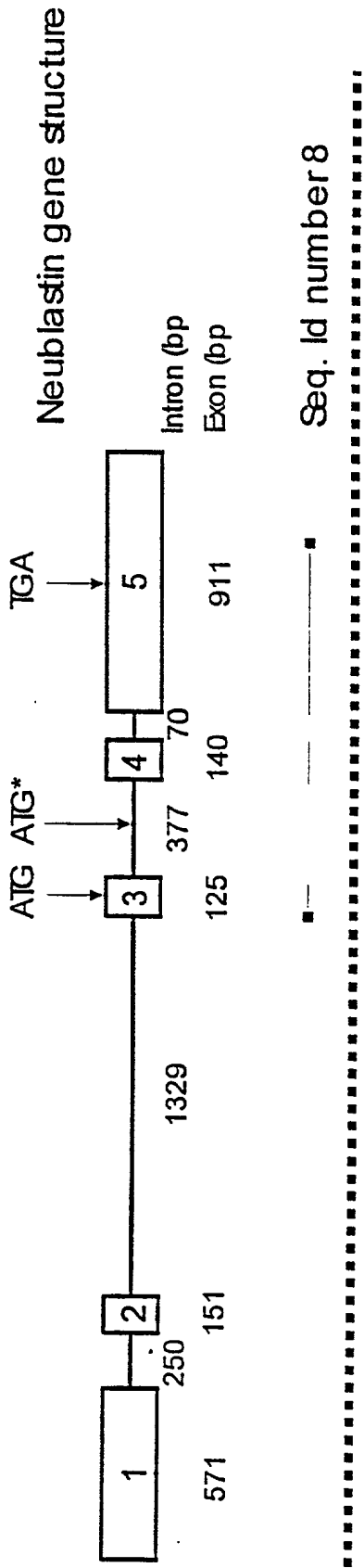
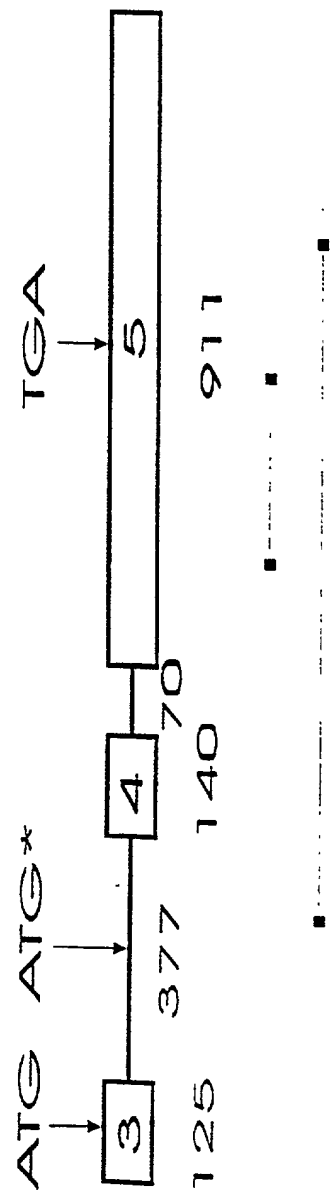


Fig. 7

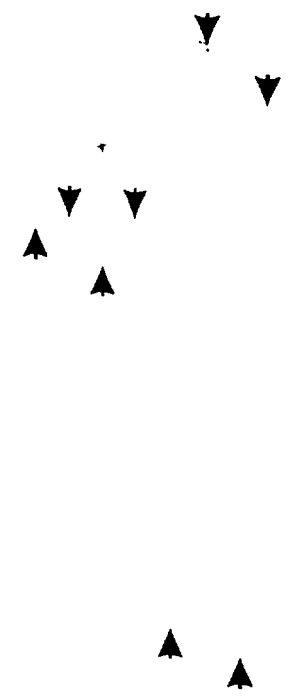


290 bp fragment identified in TBLASTN search

Genomic neublastin sequence amplified

NBN primers

- Seq. Id number 17
- Seq. Id number 18
- Seq. Id number 21
- Seq. Id number 22
- Seq. Id number 23
- Seq. Id number 24
- Seq. Id number 25
- Seq. Id number 26



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Alignment of Neublastin primers used in Rapid-Screen with
homologous regions in other GDNF ligands

5' -C CTG GCC AGC CTA CTG GG-3'	SEQ ID No 17
G CTG GCC CGG CTG CAG GG	persephin
G CTG CGA CGA CTG CGC CA	neurturin
A TTG AAA AAC TTA TCC AG	GDNF

5' -AA GGA GAC CGC	TTC GTA GCG-3'	SEQ ID No 18
TA GGC CAC GTC	GGT GTA GCG	persephin
AA GGA CAC CTC GTC CTC GTA GGC		neurturin
AA CGA CAG GTC ATC ATC AAA GGC		GDNF

conserved nucleotides shown in bold

Fig. 8

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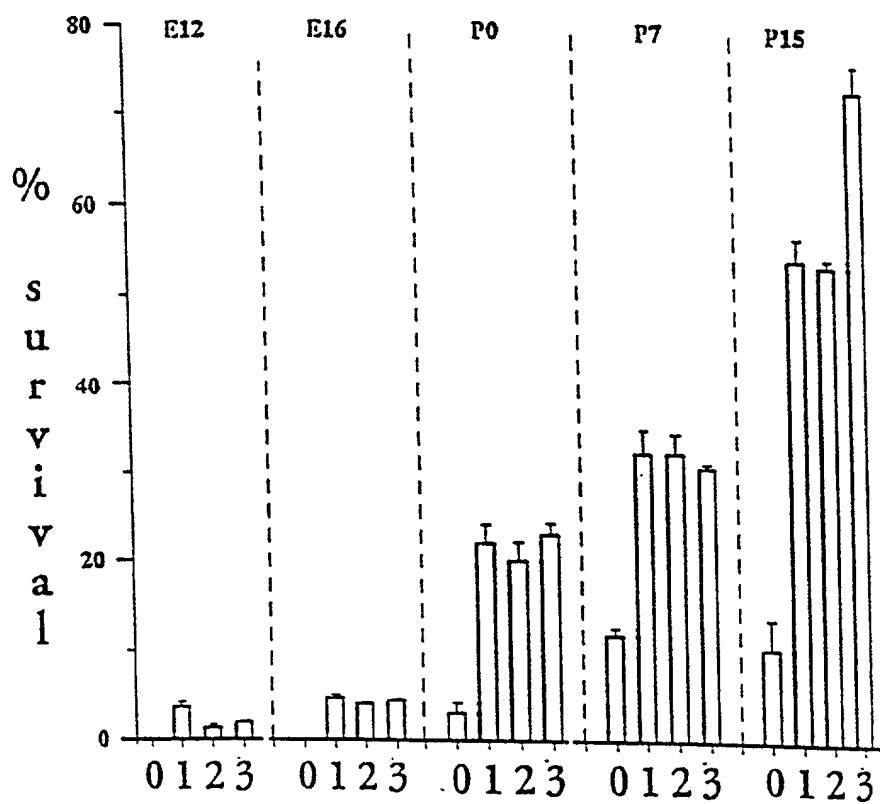
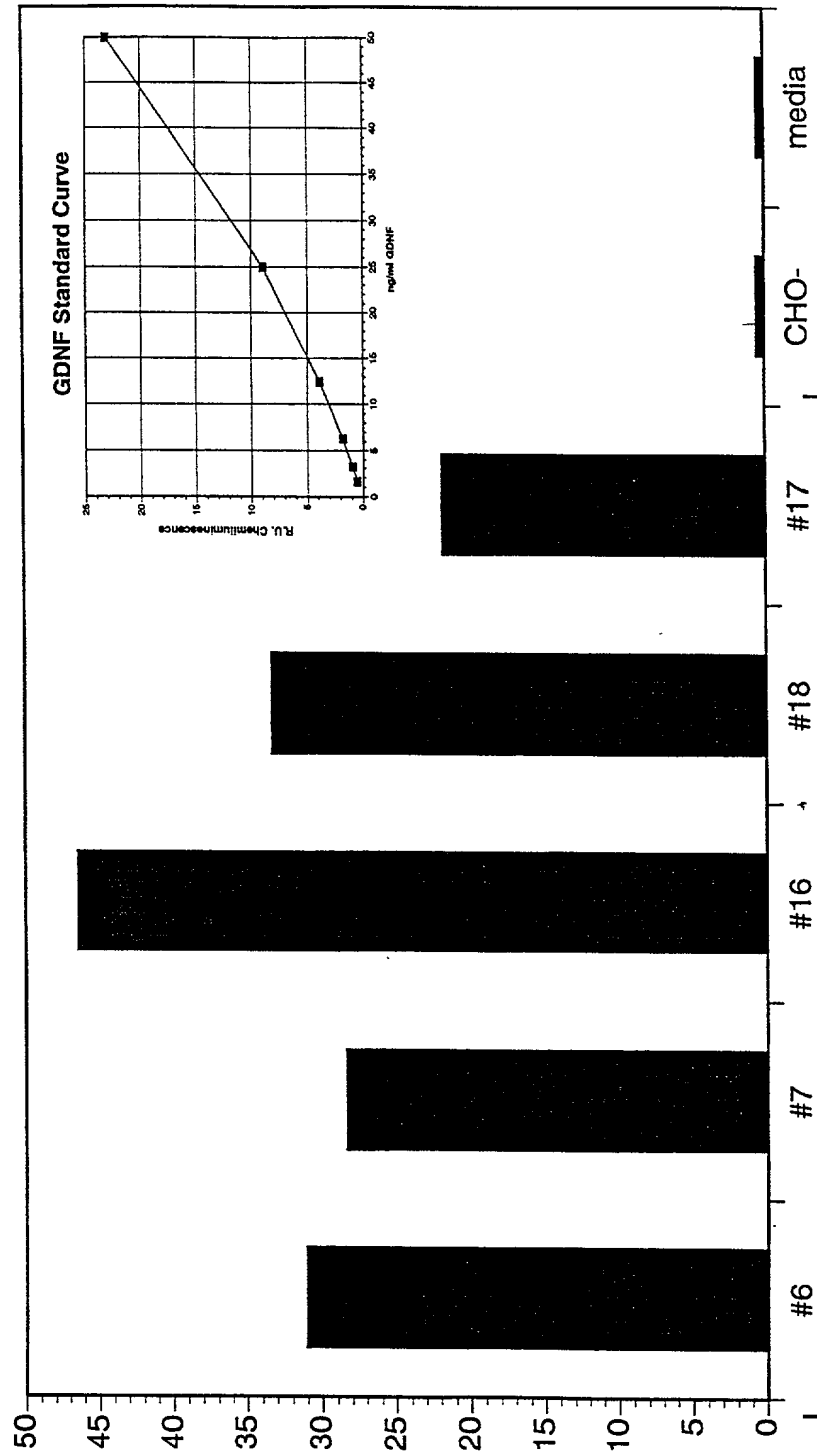


Fig. 9

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Estimated Neublastin Concentration [ng/ml]



CHO Neblastin Clones

Fig. 10

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Relative Chemiluminescence Units (R.U.)

(Off Scale, ~50R.U.)

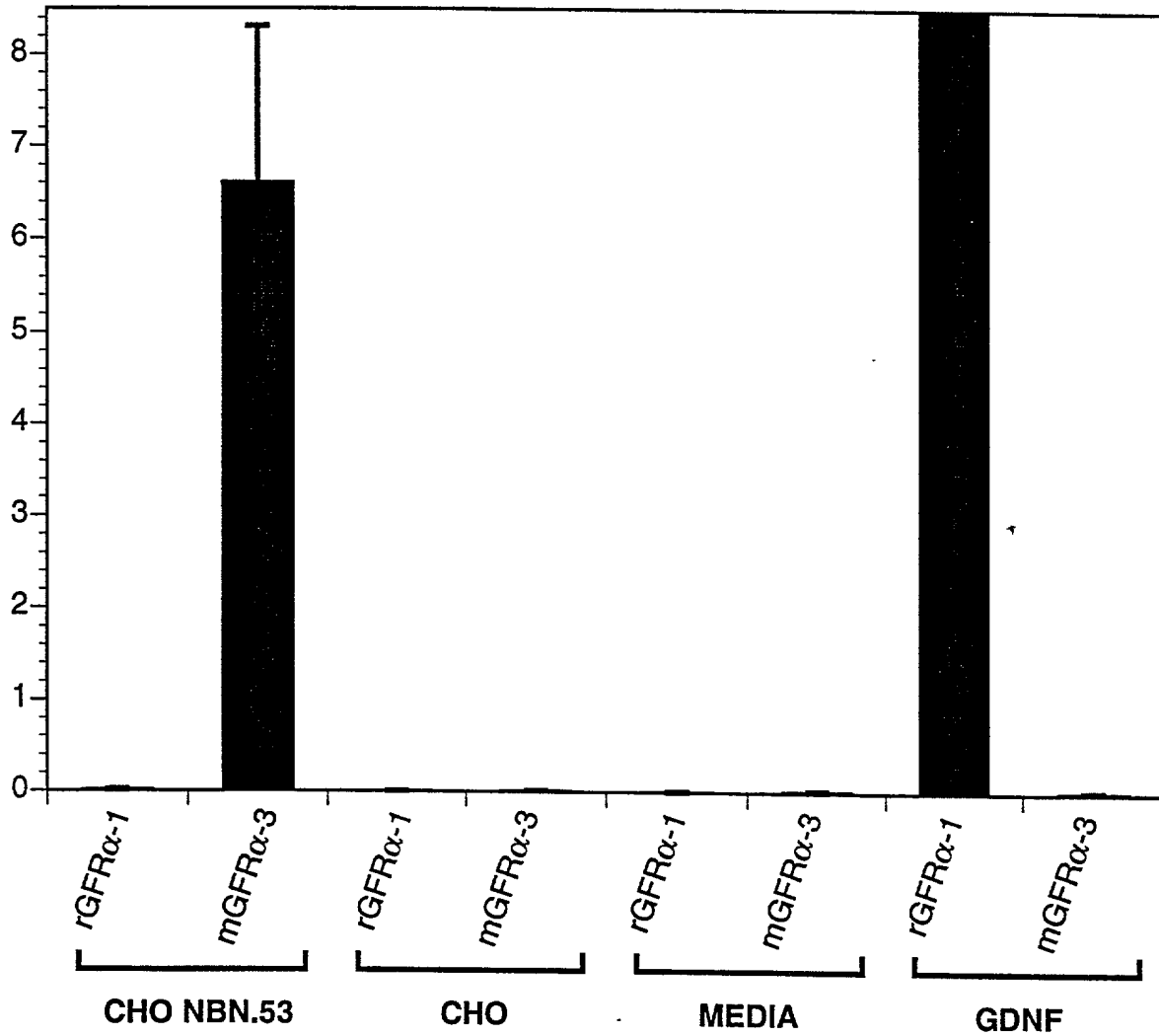
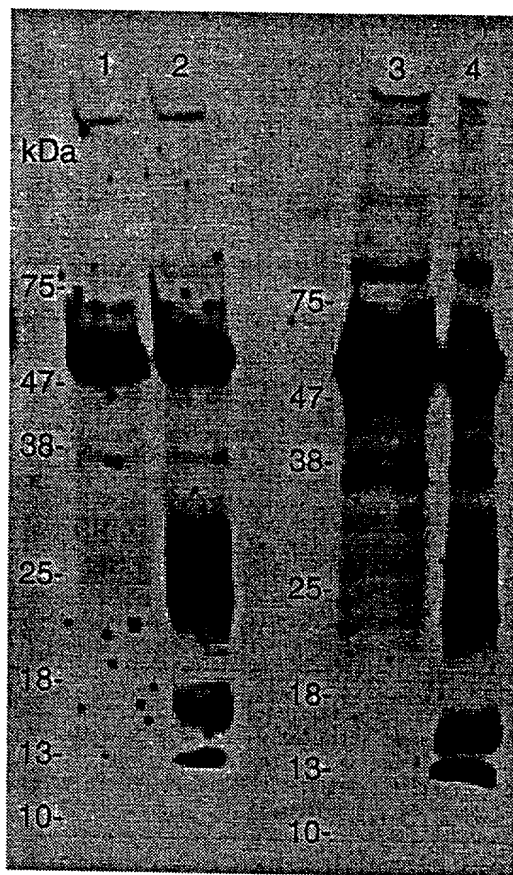
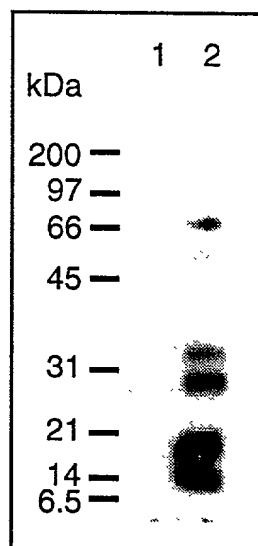


Fig. 11



1. Control medium stained with R30 anti-peptide antibody
2. Neublazin containing conditioned medium stained with R30 anti-peptide antibody
3. Control medium stained with R31 anti-peptide antibody
4. Neublazin containing conditioned medium stained with R31 anti-peptide antibody

Fig. 12



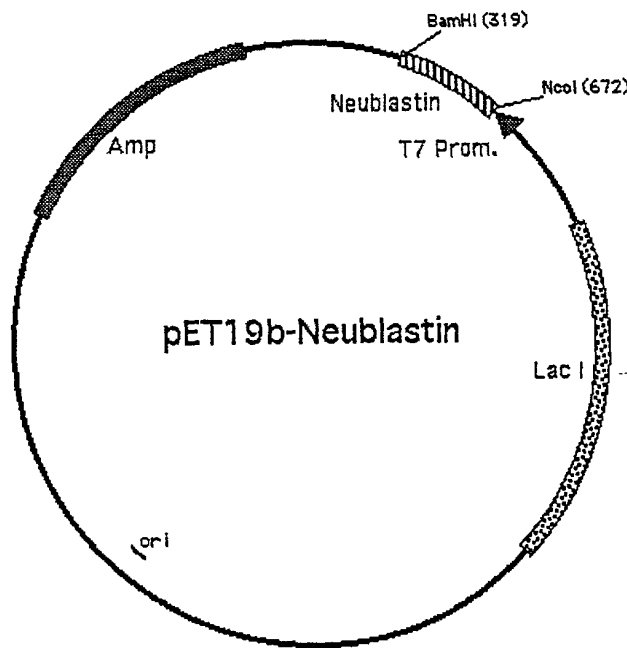
Extraction of neublastin by affinity-binding on RETL3-Ig

Lane 1: bound from CHO control conditioned media

Lane 2: bound from neublastin overexpressing CHO conditioned media

Fig. 13

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Neubl原因 Syngene

NcoI (318)

316 TACCATGGCT GGAGGACCGG GATCTCGTGC TCGTGCAGCA GGAGCACGTG GCTGTCGTCT
ATCTTACCGA CCTCCTGGCC CTAGAGCACG AGCACGTCGT CCTCGTGCAC CGACAGCAGA
1▶ M A G G P G S R A R A A G A R G C R L

376 GCGTTCTCAA CTAGTGCCGG TCGTGCACCT CGGACTGGGA CACCGTTCCG ACGAACTAGT
CGCAAGAGTT GATCACGGCC ACGCACGTGA GCCTGACCCT GTGGCAAGGC TGCTTGATCA
19▶ R S Q L V P V R A L G L G H R S D E L V

436 ACGTTTTTCGT TTTTGTTCAG GATCTTGTGC TCGTGCACGT TCTCCGCATG ATCTATCTCT
TGCAAAAGCA AAAACAAGTC CTAGAACAGC AGCACGTGCA AGAGGCGTAC TAGATAGAGA
39▶ R F R F C S G S C R R A R S P H D L S L

496 AGCATCTCTA CTAGGAGCCG GAGCACTAAG ACCGCCGCCG GGATCTAGAC CTGTATCTCA
TCGTAGAGAT GATCCTCGGC CTCGTGATTC TGGCGGCGGC CCTAGATCTG GACATAGAGT
59▶ A S L L G A G A L R P P P G S R P V S Q

556 ACCTTGTTGT AGACCTACTA GATACGAAGC AGTATCTTTC ATGGACGTAA ACTCTACATG
TGGAACAACA TCTGGATGAT CTATGCTTCG TCATAGAAAG TACCTGCATT TGAGATGTAC
79▶ P C C R P T R Y E A V S F M D V N S T W

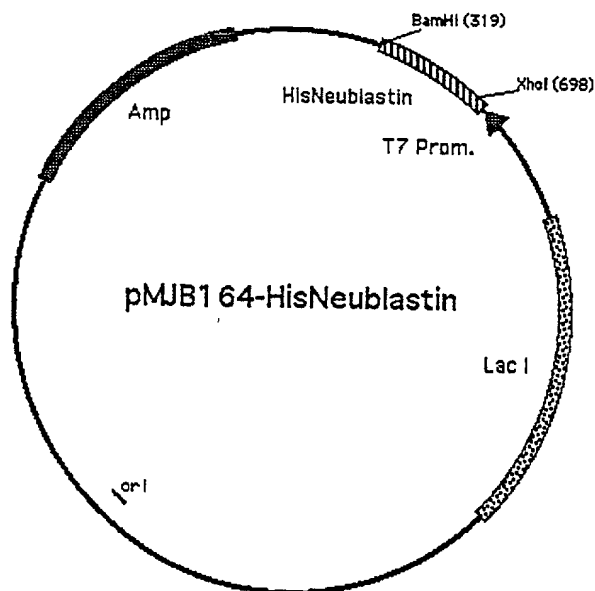
BamHI (671)

616 GAGAACCGTA GATAGACTAT CTGCAACCGC ATGTGGCTGT CTAGGATGAT AATAGGGATC
CTCTTGGCAT CTATCTGATA GACGTTGGCG TACACCGACA GATCCTACTA TTATCCCTAG
99▶ R T V D R L S A T A C G C L G . . .

676 CGGCT
GCCGA

Fig. 14

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HisNeublastin

XhoI (340)

301 TACCATGGGC CATCATCATC ATCATCATCA TCATCATCAC TCGAGCGGCC ATATCGACGA
ATCTTACCCG GTAGTAGTAG TAGTAGTAGT AGTAGTAGTG AGCTCGCCGG TATAGCTGCT
1 M G H H H H H H H H H H S S G H I D D

361 CGACGACAAG GCTGGAGGAC CGGGATCTCG TGCTCGTGCA GCAGGAGCAC GTGGCTGTCTG
GCTGCTGTTC CGACCTCCTG GCCCTAGAGC ACGAGCACGT CGTCCTCGTG CACCGAČAGC
19 D D K A G G P G S R A R A A G A R G C R

421 TCTGCGTTCT CAACTAGTGC CGGTGCGTGC ACTCGGACTG GGACACCGTT CCGACGAACT
AGACGCAAGA GTTGATCACG GCCACGCACG TGAGCCTGAC CCTGTGGCAA GGCTGCTTGA
39 L R S Q L V P V R A L G L G H R S D E L

481 AGTACGTTTT CGTTTTTGTG CAGGATCTTG TCGTCGTGCA CGTTCTCCGC ATGATCTATC
TCATGCAAAA GCAAAAACAA GTCCTAGAAC AGCAGCACGT GCAAGAGGCG TACTAGATAG
59 V R F R F C S G S C R R A R S P H D L S

541 TCTAGCATCT CTACTAGGAG CCGGAGCACT AAGACCGCCG CCGGGATCTA GACCTGTATC
AGATCGTAGA GATGATCCTC GGCCTCGTGA TTCTGGCGGC GGCCCTAGAT CTGGACATAG
79 L A S L L G A G A L R P P P G S R P V S

601 TCAACCTTGT TGTAGACCTA CTAGATACGA AGCAGTATCT TTCATGGACG TAAACTCTAC
AGTTGGAACA ACATCTGGAT GATCTATGCT TCGTCATAGA AAGTACCTGC ATTTGAGATG
99 Q P C C R P T R Y E A V S F M D V N S T

BamHI (719)

661 ATGGAGAACC GTAGATAGAC TATCTGCAAC CGCATGTGGC TGTCTAGGAT GATAATAGGG
TACCTCTTGG CATCTATCTG ATAGACGTTG GCGTACACCG ACAGATCCTA CTATTATCCC
119 W R T V D R L S A T A C G C L G . .

721 ATCCGGCTGC TAACAAAGCC CG
TAGGCCGACG ATTGTTTCGG GC

Fig. 15

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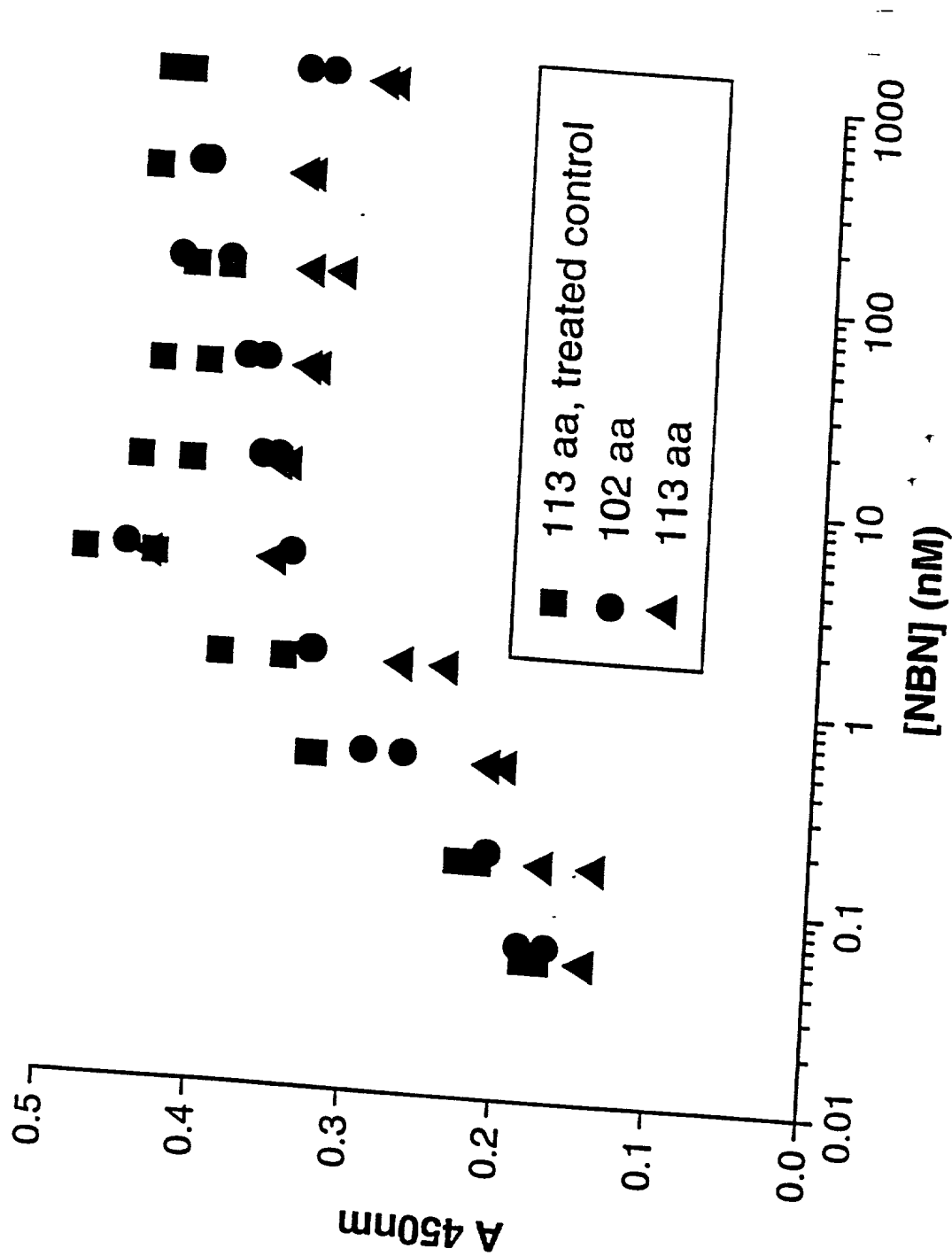


FIG. 16

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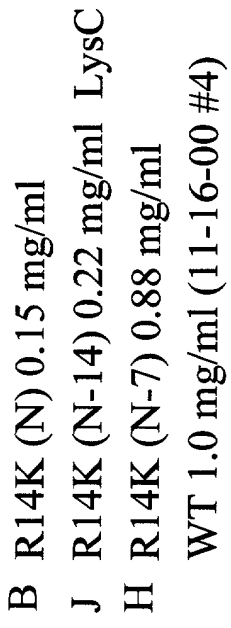


FIG. 17